

10/539634

RAW SEQUENCE LISTING

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Application Serial Number: 10/539634
Source: PCT
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PCT

RAW SEQUENCE LISTING

DATE: 06/27/2005

PATENT APPLICATION: US/10/539,634

TIME: 10:38:37

Input Set : A:\SEQ LIST WSU-10 (US).txt
 Output Set: N:\CRF4\06272005\J539634.raw

3 <110> APPLICANT: CARLOCK, Leon
 4 CYPHER, Maria
 6 <120> TITLE OF INVENTION: Bioactive Peptides and Unique IRES Elements from
 7 Myelin Proteolipid Protein PLP/DM20
 9 <130> FILE REFERENCE: 2872-0010
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,634
 C--> 12 <141> CURRENT FILING DATE: 2005-06-16
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/39873
 15 <151> PRIOR FILING DATE: 2003-12-16
 17 <150> PRIOR APPLICATION NUMBER: US 60/433,573
 18 <151> PRIOR FILING DATE: 2002-12-16
 20 <160> NUMBER OF SEQ ID NOS: 40
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 850
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(831)
 34 <400> SEQUENCE: 1
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 37 1 5 10 15
 39 gct tcc ctg gtg gcc act gga ttg tgt ttc ttt ggg gtg gca ctg ttc 96
 40 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe
 41 20 25 30
 43 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag 144
 44 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
 45 35 40 45
 47 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg 192
 48 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
 49 50 55 60
 51 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc 240
 52 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
 53 65 70 75 80
 55 ctt tat ggg gcc ctc ctg gct gag ggc ttc tac acc acc ggc gca 288
 56 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
 57 85 90 95
 59 gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc 336
 60 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
 61 100 105 110
 63 ctg agc gca acg gta aca ggg ggc cag aag ggg agg ggt tcc aga ggc 384

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64	Leu	Ser	Ala	Thr	Val	Thr	Gly	Gly	Gln	Lys	Gly	Arg	Gly	Ser	Arg	Gly
65	115				120					125						
67	caa	cat	caa	gct	cat	tct	ttg	gag	cgg	gtg	tgt	cat	tgt	ttg	gga	aaa
68	Gln	His	Gln	Ala	His	Ser	Leu	Glu	Arg	Val	Cys	His	Cys	Leu	Gly	Lys
69	130				135					140						
71	tgg	cta	gga	cat	ccc	gac	aag	ttt	gtg	ggc	atc	acc	tat	gcc	ctg	acc
72	Trp	Leu	Gly	His	Pro	Asp	Lys	Phe	Val	Gly	Ile	Thr	Tyr	Ala	Leu	Thr
73	145				150				155				160			
75	gtt	gtg	tgg	ctc	ctg	gtg	ttt	gcc	tgc	tct	gct	gtg	ccc	gtg	tac	att
76	Val	Val	Trp	Leu	Leu	Val	Phe	Ala	Cys	Ser	Ala	Val	Pro	Val	Tyr	Ile
77					165				170				175			
79	tac	ttc	aac	acc	tgg	acc	acc	tgc	gac	tct	att	gcc	ttc	ccc	agc	aag
80	Tyr	Phe	Asn	Thr	Trp	Thr	Thr	Cys	Asp	Ser	Ile	Ala	Phe	Pro	Ser	Lys
81					180				185				190			
83	acc	tct	gcc	agt	ata	ggc	agt	ctc	tgt	gct	gac	gcc	aga	atg	tat	ggt
84	Thr	Ser	Ala	Ser	Ile	Gly	Ser	Leu	Cys	Ala	Asp	Ala	Arg	Met	Tyr	Gly
85					195				200				205			
87	gtt	ctc	cca	tgg	aat	gct	ttc	cct	ggc	aag	gtt	tgt	ggc	tcc	aac	ctt
88	Val	Leu	Pro	Trp	Asn	Ala	Phe	Pro	Gly	Lys	Val	Cys	Gly	Ser	Asn	Leu
89					210				215				220			
91	ctg	tcc	atc	tgc	aaa	aca	gct	gag	ttc	caa	atg	acc	ttc	cac	ctg	ttt
92	Leu	Ser	Ile	Cys	Lys	Thr	Ala	Glu	Phe	Gln	Met	Thr	Phe	His	Leu	Phe
93	225				230				235				240			
95	att	gct	gca	ttt	gtg	ggg	gct	gca	gct	aca	ctg	gtt	tcc	ctg	ctc	acc
96	Ile	Ala	Ala	Phe	Val	Gly	Ala	Ala	Ala	Thr	Leu	Val	Ser	Leu	Leu	Thr
97					245				250				255			
99	ttc	atg	att	gct	gcc	act	tac	aac	ttt	gcc	gtc	ctt	aaa	ctc	atg	ggc
100	Phe	Met	Ile	Ala	Ala	Thr	Tyr	Asn	Phe	Ala	Val	Leu	Lys	Leu	Met	Gly
101					260				265				270			
103	cga	ggc	acc	aag	ttc	tgatacactg	gtttccctg									850
104	Arg	Gly	Thr	Lys	Phe											
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116	1				5				10				15			
118	Ala	Ser	Leu	Val	Ala	Thr	Gly	Leu	Cys	Phe	Phe	Gly	Val	Ala	Leu	Phe
119					20				25				30			
121	Cys	Gly	Cys	Gly	His	Glu	Ala	Leu	Thr	Gly	Thr	Glu	Lys	Leu	Ile	Glu
122					35				40				45			
124	Thr	Tyr	Phe	Ser	Lys	Asn	Tyr	Gln	Asp	Tyr	Glu	Tyr	Leu	Ile	Asn	Val
125					50				55				60			
127	Ile	His	Ala	Phe	Gln	Tyr	Val	Ile	Tyr	Gly	Thr	Ala	Ser	Phe	Phe	Phe
128	65				70				75				80			
130	Leu	Tyr	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Phe	Tyr	Thr	Thr	Gly	Ala	
131					85				90				95			

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Input Set : A:\SEQ LIST WSU-10 (US).txt
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133 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
 134 100 105 110
 136 Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly
 137 115 120 125
 139 Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys
 140 130 135 140
 142 Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr
 143 145 150 155 160
 145 Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile
 146 165 170 175
 148 Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys
 149 180 185 190
 151 Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly
 152 195 200 205
 154 Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu
 155 210 215 220
 157 Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe
 158 225 230 235 240
 160 Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr
 161 245 250 255
 163 Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly
 164 260 265 270
 166 Arg Gly Thr Lys Phe
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 173 <213> ORGANISM: Homo sapiens
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 176 <221> NAME/KEY: CDS
 177 <222> LOCATION: (1)..(726)
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 182 1 5 10 15
 184 gct tcc ctg gtg gcc act gga ttg tgt ttc ttt ggg gtg gca ctg ttc 96
 185 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe
 186 20 25 30
 188 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag 144
 189 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
 190 35 40 45
 192 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg 192
 193 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
 194 50 55 60
 196 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc ttc 240
 197 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
 198 65 70 75 80
 200 ctt tat ggg gcc ctc ctg ctg gct gag ggc ttc tac acc acc ggc gca 288
 201 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Gly Ala

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204 gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc				336
205 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly				
206 100	105	110		
208 ctg agc gca acg ttt gtg ggc atc acc tat gcc ctg acc gtt gtg tgg				384
209 Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp				
210 115	120	125		
212 ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att tac ttc aac				432
213 Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn				
214 130	135	140		
216 acc tgg acc acc tgc gac tct att gcc ttc ccc agc aag acc tct gcc				480
217 Thr Trp Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala				
218 145	150	155	160	
220 agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt gtt ctc cca				528
221 Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro				
222 165	170	175		
224 tgg aat gct ttc cct ggc aag gtt tgt ggc tcc aac ctt ctg tcc atc				576
225 Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile				
226 180	185	190		
228 tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt att gct gca				624
229 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala				
230 195	200	205		
232 ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc acc ttc atg att				672
233 Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile				
234 210	215	220		
236 gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg ggc cga ggc acc				720
237 Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly Arg Gly Thr				
238 225	230	235	240	
240 aag ttc tga				729
241 Lys Phe				
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245 <211> LENGTH: 242				
246 <212> TYPE: PRT				
247 <213> ORGANISM: Homo sapiens				
249 <400> SEQUENCE: 4				
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254 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe				
255 20	25	30		
257 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu				
258 35	40	45		
260 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val				
261 50	55	60		
263 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe				
264 65	70	75	80	
266 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala				
267 85	90	95		
269 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly				
270 100	105	110		

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272 Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp
 273 115 120 125
 275 Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn
 276 130 135 140
 278 Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala
 279 145 150 155 160
 281 Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro
 282 165 170 175
 284 Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile
 285 180 185 190
 287 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala
 288 195 200 205
 290 Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile
 291 210 215 220
 293 Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly Arg Gly Thr
 294 225 230 235 240
 296 Lys Phe
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 300 <211> LENGTH: 216
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 302 <213> ORGANISM: Homo sapiens
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 305 <221> NAME/KEY: CDS
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 311 1 5 10 15
 313 tcc aac ctt ctg tcc atc tgc aaa aca gct gag ttc caa atg acc ttc 96
 314 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe
 315 20 25 30
 317 cac ctg ttt att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc 144
 318 His Leu Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser
 319 35 40 45
 321 ctg ctc acc ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa 192
 322 Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys
 323 50 55 60
 325 ctc atg ggc cga ggc acc aag ttc 216
 326 Leu Met Gly Arg Gly Thr Lys Phe
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 331 <211> LENGTH: 72
 332 <212> TYPE: PRT
 333 <213> ORGANISM: Homo sapiens
 335 <400> SEQUENCE: 6
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 340 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe
 341 20 25 30

VERIFICATION SUMMARY

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Input Set : A:\SEQ LIST WSU-10 (US).txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date